

BLASTX ALIGNMENT OF SEQ ID NO: 4 LEUCINE-RICH REPEAT PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS LRR PROTEIN-LIKE) WITH HUMAN GARP PROTEIN PRECURSOR PROTEIN SEQ ID NO: 19

Query: Leucine-rich repeat-like protein (SEQ ID 4)
 Sbjct: Human Garp protein precursor protein g1|5031707 ref|NP_005503.1| glycoprotein A repetitions predominant precursor; garpin >sp|Q14392|GARP HUMAN GARP PROTEIN PRECURSOR (GARPIN) >pir||S42799 garp precursor - human emb|CAA80847.1| (Z24680) garp [Homo sapiens] (SEQ ID NO: 19)
 length = 662

Score = 822 (289.4 bits), Expect = 4.9e-81, P = 4.9e-81
 Identities = 245/637 (38%), Positives = 328/637 (51%)

Query: 267 CKLVGGADCRGQSLASVPSLPPHARMLTLDANPLKTLWNHSLQPYPLLESLSHSCHL 446
 CK+V C+ L VPS LPP L L N L+++ L Y L L L + +
 Sbjct: 26 CKWVDKVKSCQVLGILLQVPVLPDPTETLIDSGNQLRSILASPLGFYTA LRHLDISTNEI 85

Query: 447 ERISRGAFQEQGHLRSVLGDNCISENYEETAALHALPGLRRIDLSGNALTEDMALML 626
 + GAFQ HL L L N L+ +A L LP + LIDSGN+L + +L
 Sbjct: 86 SFLQPGAFQALTHLEHLAHNRRLAMATASAGGLGPLPRVTSIDLSGNSLYSGLLERLL 145

Query: 627 QNLSLRSVSLAGNTIMRLDSDVFEGLERLELDLQRYIFETEGGAFDGLAELRLHNL 806
 SL ++SLA N++ RL F + L +LDL N + +IE GAF+GL L HNL+
 Sbjct: 146 GEAPSLHTLSLAENSLTRLTRHTFRDMPALAEQLDHSNVLMDIEDGAFEGLPRLTHNL 205

Query: 807 FNNLPCIVDFGLTRLRVIANVSYNVLWMF-LATGGEAFELFETLIDLSHNQLFPPLLPQYS 983
 N+L CI DF L +LRVL++S N +E F A+ +A F+L LDL N+LL FP L
 Sbjct: 206 RNSLTCTISDFSLQQLRVLDLSCNSIEAFQTASQPAEFQLTWLDLRENKILHFPDLAALP 265

Query: 984 KLRLLLRDNNMGFYRDLYNTSSPREMVAQFLAVDG-NVTNITTVSLWEEFSSSDIADLR 1160
 +L L L NN+ R T P++ +G + ++ S L+ L
 Sbjct: 266 RLILYLNL-SNNL--IR--LPTGPPQDSKGIHAPSEGSALPLSAPS--GNASGRPLSQLL 318

Query: 1161 FIDMSQNFQYLPDGFRLKMPSLSHLNLHONCLMTLHIREHPPGALTELDLSHNQISEL 1340
 ID+S N+ + +PD FL + SL LNL +NCL T R L IDLSHN L L
 Sbjct: 319 NIDLSYNEIELIPDSFLEHLTSLCFLNLSRNCLRTFEARRLGSLPCMILDLDSHNALETL 378

Query: 1341 HLAPGLASCLGSLRLFNLSNQLLGVPPGILFANARNITTLIDMSHNQISLCPPLPAASDRV 1520
 L A LGSIR L N L +PP FAN ++ L++ N++S C P D G
 Sbjct: 379 ELG---ARALGSLRTLLQGNALRDLPPYTFANLASLQRLNLQGNRVSPCGGP---DEPG 432

Fig. 1A

BLASTX ALIGNMENT OF SEQ ID NO: 4 LEUCINE-RICH REPEAT PROTEIN-LIKE POLYPEPTIDE
(IDENTIFIED AS LRR PROTEIN-LIKE) WITH HUMAN GARP PROTEIN PRECURSOR PROTEIN SEQ
ID NO: 19

Query: 1521 PPSCVDFRNMASLSLSLEGCGALPDPCFQGTSLTYLDLSSNMG--VLNGSLAPLDV 1694
P CV F + SLRSLSL + L F T LT LDLSN G V G+L L+
Sbjct: 433 PSGCVAFSGITSLRSLSLVDNEIELLRAGAFHTPLTELDLSSNPGLEVAATGALGLE-- 490

Query: 1695 APMLOVLSLRNMGHSSFMALDFSGFGLRDLDLSGNCLPIFFRFGSLAETLDLRNS 1874
L+VL+L+ GL + +D F L+ L+L+ N L P + +++LE LDLR NS
Sbjct: 491 -ASLEVLALQNGNL--MVLQVDLPFCFICKRLNLAENRLSHLPAMTQAVSLEVLDLRNS 547

Query: 1875 LTALPQKAVSEQLSRGLRTIYLSNPYPDCCGVGWMGALQ-H-GQTVADWAM-VTCNLSSK 2045
+ LP A+ L LR +YL NP CCG +GW A Q H G+ D + C SS+
Sbjct: 548 FSLPFSAMG-LETSLRRLYLQGNPLSCCG-NGWLAQAQHQGRVDVDAIQDILICRFSSQ 605

Query: 2046 IIRVTELPQGVPRDCKWERL-DLGILY-LVLILPSC--LTLVACTVI 2177
L P DC+ L ++ L+ L IL S LT L AC +
Sbjct: 606 --EEVSLSHVRPEDECKGGLKNINLIIILTFILVSAIILLTTLAACCV 651

FIG. 1B

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BLASTX ALIGNMENT OF SEQ ID NO: 4 LEUCINE-RICH REPEAT PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS LRR PROTEIN-LIKE) WITH HUMAN GLYCOPROTEIN V PROTEIN SEQ ID NO: 21

Query: Leucine-rich repeat-like protein (SEQ ID 4)
 Sbjct: gi|4758460 ref|NP_004479.1| glycoprotein V (platelet) >sp|P40197|GPV HUMAN PLATELET GLYCOPROTEIN V PRECURSOR (GPV) (CD42d) >pir||A60164 platelet membrane glycoprotein V precursor - human >pir||A47507 platelet membrane glycoprotein V precursor - human emb|CAA80637.1| (Z23091) platelet glycoprotein V precursor [Homo sapiens] >gb|AAA03069.1| (L11238) platelet membrane glycoprotein V [Homo sapiens] (SEQ ID NO: 21)
 length = 560

Score = 273 (96.1 bits), Expect = 2.8e-20, Sum P(2) = 2.8e-20
 Identities = 127/386 (32%), Positives = 177/386 (45%)

Query: 837 GLTRLRVLNVSVLEWFLATGGEA-AFELETLDSLHNQLEFP-ILPQYSKRLTLR 1007
 G+T L+ L +S + + +A G + +L+TL LS N++ P LL + L L L
 Sbjct: 72 GMTVLQRLMISDSHS-AVAPGTFSDLIKIKTLRLSRNKITHLPGALDRKWLLEQLFL- 129

Query: 1008 DNNMGFYRDLVNTSSPREMVAQFLVDGNVTNITTVSLWEFFSSDLADLRFLLDMSQNF 1187
 D+N R + + + Q L ++ N + SL+ ++L +L+ LD+S N
 Sbjct: 130 DHNA--LRGIDQNMFPQKLVNLQELALNQNLDFLPASLF-----TNLENLKLDDLSGNNL 182

Query: 1188 QYLPDGFRLKMPSLSHLNLHONCINTLHIREHEPPGALTELDLSHNQLSLHLAPGLASC 1367
 +LP G L L L LH N L++L GATTEL N + +APG
 Sbjct: 183 THLPKGLLGAQAKLERLLHSHNRLVSLDGLNSLGLALTELPFRHNRHSI--APGAFDR 240

Query: 1368 LGSRLRFNLSSNQLGVPPGLFANARNITTTIDMSHNQISLCPPLAASDRVGPSCVDFRN 1547
 L+L LS N L +P LF ++ N+T L + N L LP V F
 Sbjct: 241 LPNLSSLTSLSRNHLAFLPSALFLHSHNLTLLTFENP--LAELPG-----VLFGE 288

Query: 1548 MASLRSLSEGGGLGALPDCPFQGTSLTYLD--LSSNWGVL--NGSLAPLDVAPMLQVL 1715
 M L+ L L L LP F+ S L YL LS L G+ L + LQVL
 Sbjct: 289 MGLQELWLNRTQLRTPAALFRNLRLRYLGVTLSPRLSALPGAFQGLGE---LQVL 344

Query: 1716 SLRNMGLHSSFMALDFSGFNLRLDLSGNCLPIFDR--FGSLALETLDLRNSLTALP 1889
 +L + GL + L G G LR + L N L PR F +LE++ L N L LP
 Sbjct: 345 ALHSNGLTALPDGL-LRGLGKLRQVSLRRNRLRALPRALFRNLSSLESVQLDHNQLETLF 403

Query: 1890 QKAVSEQLSRGLRTIYLSQNPYDC-CGYD--GMGALQH 1994
 V L R L + L N + C CG+ GW OH
 Sbjct: 404 GD-VFGALPR-LTEVLLGHNSWRCDCGLGPFLLGW-LRQH 439

FIG. 3

09672221.092700

BLASTX ALIGNMENT OF SEQ ID NO: 4 LEUCINE-RICH REPEAT PROTEIN-LIKE POLYPEPTIDE
(IDENTIFIED AS LRR PROTEIN-LIKE) WITH WD-40 DOMAIN CONTAINING INSULIN-LIKE
GROWTH FACTOR BINDING PROTEIN SEQ ID NO: 22

Query: Leucine-rich repeat-like protein (SEQ ID 4)
Sbjct: sp|R85888|R85888 WD-40 domain-contg. insulin-like growth factor binding protein (SEQ ID NO: 22)
Length = 605

Score = 293 (103.1 bits), Expect = 7.3e-22, P = 7.3e-22
Identities = 141/467 (30%), Positives = 208/467 (44%)

Query: 198 GFHFLTVGWRNRSQTATAAQGVCKLVGGAADCRGQSLASV-PSSLPPHARM--LTLDAN 368
G L + N S AA Q + L G + +G L S+ P +L + L L+ N
Sbjct: 75 GTQALMLDGNNTSSVPPAFQNLSSL--GFNLQGGQLGLEPQALLGLENLCHLHLERN 132

Query: 369 PLKTLMNHSLQPYPLLESLSHSCHLERISRGAFQEQGHLRSIVIGDNCISENVEETAA 548
L++L + P L SL L + L R+ G F+ G L L LG N L+ + AA
Sbjct: 133 QLRSLALGTFAHTPALASLGLSNRRLSRLLEDGLFEGLSLMDNLGWNLSLAVLPD--AA 189

Query: 549 LHALPGLRRDLSSGNALTEDMAALMLQNLSSLSVSLAGNTIMRLDDSVFEGELRLRLD 728
L LR L L+GN L AL L+ LR + L+ N + + +VF L RL++L
Sbjct: 190 FRGLGSLREIVLAGNRLAYIQPALF-SGLAEIARELDLSRNALRAIKANVFQQLPRLQKLY 248

Query: 729 LQENYIFEIEGAFDGLAEIRHNLAFNNLPCTVD--F-GLTRRLVNLVSYNVLEWFIAT 899
L RN I + GAF GL LR L+L+ N + +++ F GL LRVL +S+N +
Sbjct: 249 LDRNLIAAVAPGAFGLKALKALRWLDLSHNRVAGLLEDTFPGILLGLRVLRLSHNAIASLRPR 308

Query: 900 GGEAFAFELETIDLSHNQL--LFFPLLQYSKLRTLLLRDNNM-----GFYRDLYNTSSPR 1058
+ LE L L HN++ L +L L L N + G + L N +
Sbjct: 309 TFKDLHFLEELQGHNRIRQLAERSFEGLGQLEVLTLIDHNQLEVKAGAFGLTNVA--- 365

Query: 1059 EMVAQFLLVDDGNVTNITTVSLMEEFSSSDIADLRFIDMSQNFQYLPDGF LRKMPSLSHL 1238
+ + GN +L E+ L L L + + + L L
Sbjct: 366 -----VMNLGNCCLR---NLPEQVFRG-LGKLHSLHLEGSCLGRIRPHTFTGLSGLRRL 415

Query: 1239 NLHQNCLMTLHIREHEPPGALTELDLSHNQLSLHLAPGLASCIGSLRLFNLSNQLLGV 1418
L N L+ + + L ELDL+ NQL+ HL L LG L LS N+L +
Sbjct: 416 FLKDNGLVGIEQSLWGLAEELLEEDLTSNQLT--HLPHRLFGGLGKLEYLLLSNRRLAEL 473

Query: 1419 PPGLFANARNITFLDMSHNQISLCPLPASDRVGPSPSCVDFRNMAISLSLEGGGLGAL 1598
P + LD+SHN++ P + +G + RN SLR+ + + GL L
Sbjct: 474 PADALGPLQRAFWLIDVSHNRLEALPNSLIAP-LGRRLYLSLRNN-SLRTFTPQPPGLERL 531

FIG. 4

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